FIG. 1A

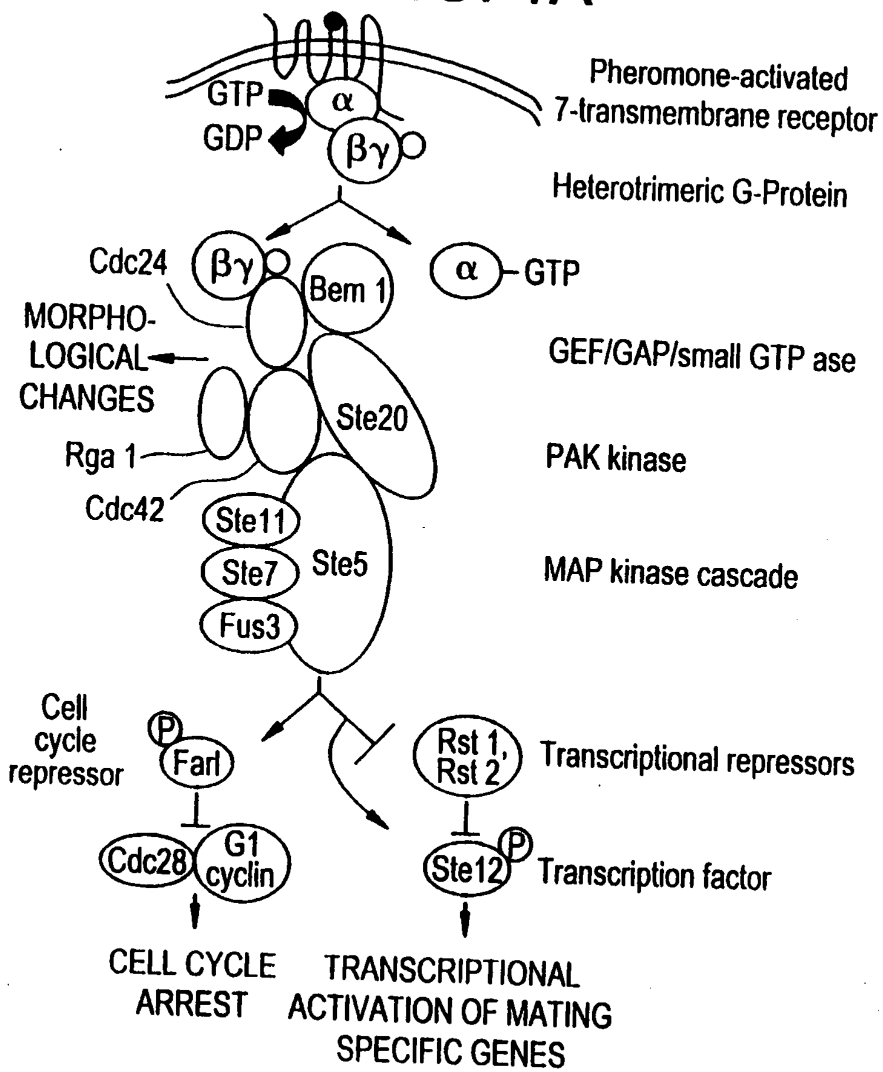

FIG. 1B

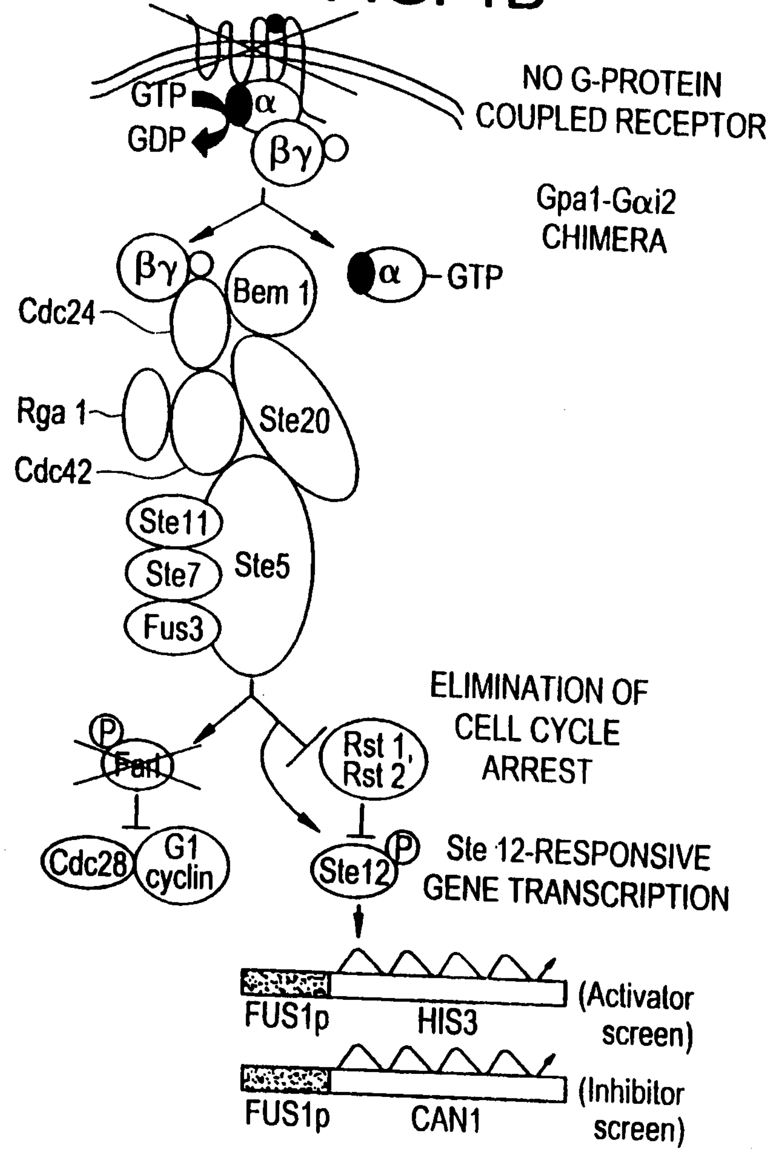

FIG. 2

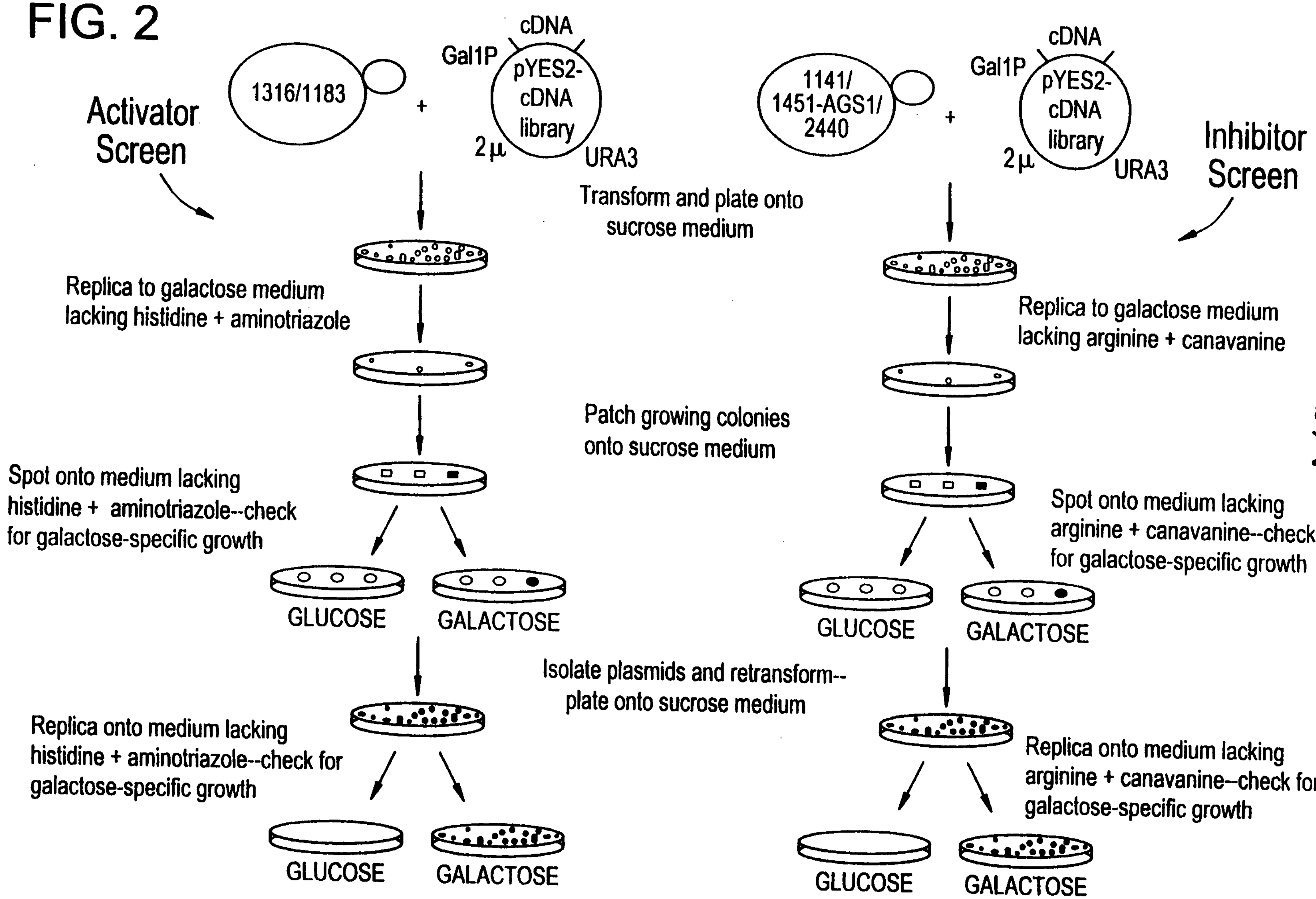

FIG. 3A

10	20	30	40	50	60	
ATGAAACTGG	CCGCGATGAT	CAAGAAGATG	TGCCCGAGCG	ACTCGGAGCT	GAGTATCCCG	60
GCCAAGAACT	GCTATCGCAT	GGTCATCCTC	GGCTCGTCCA	AGGTGGGCAA	GACGGCCATC	120
GTGTCGCGCT	TCCTCACCGG	CCGCTTCGAG	GACGCCTACA	CGCCTACCAT	CGAGGACTTC	180
CACCGCAAGT	TCTACTCCAT	CCGCGGCGAG	GTCTACCAGC	TCGACATCCT	CGACACGTCC	240
GGCAACCACC	CGTTCCCCGC	CATGCGGCGC	CTCTCCATCC	TCACAGGAGA	CGTTTTCATC	300

310	320	330	340	350	360	
CTGGTGTTCA	GTCTGGACAA	CCGCGACTCC	TTCGAGGAGG	TGCAGCGGCT	CAGGCAGCAG	360
ATCCTCGACA	CCAAGTCTTG	CCTCAAGAAC	AAAACCAAGG	AGAACGTGGA	CGTGCCCCTG	420
GTCATCTGCG	GCAACAAGGG	TGACCGCGAC	TTCTACCGCG	AGGTGGACCA	GCGCGAGATC	480
GAGCAGCTGG	TGGGCGACGA	CCCCCAGCGC	TGCGCCTACT	TCGAGATCTC	GGCCAAGAAG	540
AACAGCAGCC	TGGACCAGAT	GTTCCGCGCG	CTCTTCGCCA	TGGCCAAGCT	GCCCAGCGAG	600

610	620	630	640	650	660	
ATGAGCCCAG	ACCTGCACCG	CAAGGTCTCG	GTGCAGTACT	GCGACGTGCT	GCACAAGAAG	660
GCGCTGCGGA	ACAAGAAGCT	GCTGCGGGCC	GGCAGCGGCG	GCGGCGGCGG	CGACCCGGGC	720
GACGCCTTTG	GCATCGTGGC	ACCCTTCGCG	CGCCGGCCCA	GCGTACACAG	CGACCTCATG	780
TACATCCGCG	AGAAGGCCAG	CGCCGGCAGC	CAGGCCAAGG	ACAAGGAGCG	CTGCGTCATC	840
AGCTAG 846						

FIG.3B

MKLAAMIKKMCPSDSELSIP AKNCYRMVILGSSKVGKTAI 40

VSRFLTGRFEDAYTPTIEDF HRKFYSIRGEVYQLDILDTS 80

GNHPFPAMRRLSILTGDVFI LVFSLDNRDSFEEVQRLRQQ 120

ILDTKSCLKNKTKENVDVPL VICGNKGDRDFYREVDQREI 160

EQLVGDDPQRCAYFEISAKK NSSLDQMFRALFAMAKLPSE 200

MSPDLHRKVSVQYCDVLHKK ALRNKKLLRAGSGGGGGDPG 240

DAFGIVAPFARRPSVHSDLM YIREKASAGSQAKDKERCVI S 281

FIG.4A

```
                                    PM1               G1     PM2
C-HA-RAS1    ---------------------MTEYKLVVVGAGGVGKSALTIQLIQNHFVDEYDPTIEDS
RALA         ----------MAANKPKGQNSLALHKVIMVGSGGVGKSALTLQFMYDEFVEDYEPTKADS
RAB-1A       --------------MSSMNPEYDYLFKLLLIGDSGVGKCLLLRFADDTYTESYISTIGVD
RHOHP1       -------MTAAQAAGEEAPPGVRSVKVVLVGDGGCGKTSLLMVFADGAFPESYTPTVFER
CDC42        ---------------------MQTIKCVVVGDGAVGKTCLLISYTTNKFPSEYVPTVFDN
RAC2         ---------------------MQAIKCVVVGDGAVGKTCLLISYTTNAFPGEYIPTVFDN
ARL1         -------MGGFFSSIFSSLFGTREMRILILGLDGAGKTTILYRLQVGEVVTTI-PTIGFN
RND3/RHOE    ----------------MDPNQNVKCKIVVVGDSQCGKTALLHVFAKDCFPENYVPTVFEN
AGS1         MKLAAMIKKMCPSDSELSIPAKNCYRMVILGSSKVGKTAIVSRFLTGRFEDAYTPTIEDF
                                   : :::* .  **: :        .       .*

                     PM3
C-HA-RAS1    YRKQ-VVIDGETCLLDILDTAGQEEYSAMRDQYMRTGEGFLCVFAINNTKSFEDIHQYRE
RALA         YRKK-VVLDGEEVQIDILDTAGQEDYAAIRDNYFRSGEGFLCVFSITEMESFAATADFRE
RAB-1A       FKIRTIELDGKTIKLQIWDTAGQERFRTITSSYYRGAHGIIVVYDVTDQESFNNVKQ-WL
RHOHP1       YMVN-LQVKGKPVHLHIWDTAGQDDYDRLRPLFYPDASVLLLCFDVTSPNSFDNIFNRWY
CDC42        YAVT-VMIGGEPYTLGLFDTAGQEDYDRLRPLSYPQTDVFLVCFSVVSPSSFENVKEKWV
RAC2         YSAN-VMVDSKPVNLGLWDTAGQEDYDRLRPLSYPQTDVFLICFSLVSPASYENVRAKWF
ARL1         VET----VTYKNLKFQVWDLGGQTSIRPYWRCYYSNTDAVIYVVDSCDRDRIGISKSELV
RND3/RHOE    YTAS-FEIDTQRIELSLWDTSGSPYYDNVRPLSYPDSDAVLICFDISRPETLDSVLKKWK
AGS1         HRKF-YSIRGEVYQLDILDTSGNHPFPAMRRLSILTGDVFILVFSLDNRDSFEEVQRLRQ
                  :   : : * .*.               .:
```

FIG.4B

```
                                        G2
C-HA-RAS1    QIKRVKD--------SDDVPMVLVGNKCDLAA--------------RTVESRQAQDLARS
RALA         QILRVKE--------DENVPFLLVGNKSDLEDK-------------RQVSVEEAKNRAEQ
RAB-1A       QEIDRYA--------SENVNKLLVGNKCDLTTK-------------KVVDYTTAKEFADS
RHOHP1       PEVNHF---------CKKVPIIVVGCKTDLRKDKSLVNKLRRNGLEPVTYHRGQEMARSV
CDC42        PEITHH---------CPKTPFLLVGTQIDLRDDPSTIEKLAKNKQKPITPETAEKLARDL
RAC2         PEVRHH---------CPSTPIILVGTKLDLRDDKDTIEKLKEKKLAPITYPQGLALAKEI
ARL1         AMLEEEE--------LRKAILVVFANKQDMEQAMTSSEMANSLGLPALKDRK--------
RND3/RHOE    GEIQEF---------CPNTKMLLVGCKSDLRTDVSTLVELSNHRQTPVSYDQGANMAKQI
AGS1         QILDTKSCLKNKTKENVDVPLVICGNKGD-RDFY------------REVDQREIEQLVGD
                                      ..  :: . : *
                         G3
C-HA-RAS1    YG--IPYIETSAKTRQG-VEDAFYTLVREIR------------------------------
RALA         WN--VNYVETSAKTRAN-VDKVFFDLMREIR------------------------------
RAB-1A       LG--IPFLETSAKNATN-VEQSFMTMAAEIK------------------------------
RHOHP1       GA--VAYLECSARLHDN-VHAVFQEAAEVAL------------------------------
CDC42        KA--VKYVECSALTQRG-LKNVFDEAILAAL------------------------------
RAC2         DS--VKYLECSALTQRG-LKTVFDEAIRAVL------------------------------
ARL1         ----WQIFKTSATKGTG-LDEAMEWLVETLKSRQ
RND3/RHOE    GA--ATYIECSALQSENSVRDIF----HVATLAC---------------VNKTNKNVKRNK
AGS1         DPQRCAYFEISAKKNSS-LDQMFRALFAMAKLPSEMSPDLHRKVSVQYCDVLHKKALRNKK
                 ..: **       :     :

C-HA-RAS1    -----------------------------QHKLRKLNPPDESGPGCMSCKCVLS
RALA         -------------------------ARKMEDSKEKNGKKKRKSLAKRIRERCCIL
RAB-1A       -KRMGPGATAGGA------------------EKSNVKIQSTPVKQAGGGCC
RHOHP1       ------------------------------------SSRGRNFWRRITQGFCVVT
CDC42        ----------------------------------------EPPETQPKRKCCIF
RAC2         ----------------------------------------CPQPTRQQKRACSLL
ARL1
RND3/RHOE    SQRA------------TKRISHMPSRP--------ELSAVATDLRKDKAKSCTVM
AGS1         LLRAGSGGGGGDPGDAFGIVAPFARRPSVHSDLMYIREKASAGSQAKDKERCVIS
```

FIG.5

		P REGION		G'REGION	
RhoE/Rnd3		KIVVVGDSQCGKTALL	. . . . .	LSLWDTSGSPYYD	
Rnd2		KIVVVGDAECGKTALL	. . . . .	LNMWDTSGSSYYD	
Rnd1		KLVLVGDVQCGKTAML	. . . . .	LSLWDTSGSPYYD	
RhoA		KLVIVGDGACGKTCLL	. . . . .	LALWDTAGQEDYD	
RhoB		KLVVVGDGACGKTCLL	. . . . .	LALWDTAGQEDYD	
Cdc42		KCVVVGDGAVGKTCLL	. . . . .	LGLFDTAGQEDYD	
Rac1		KCVVVGDGAVGKTCLL	. . . . .	LGLWDTAGQEDYD	
H-ras		KLVVVGAGGVGKSALT	. . . . .	LDILDTAGQEEYD	
AGS	26	RMVILGSSKVGKTAIV	. . . . .	LDILDTSGNHPFP	86
		*		* *	